

Figure 1A

1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGCGG 60
 61 CGCCGGTGCCGACAGATGCTGGGCCAGCCGACGGCTGCTCTTCATCCTGGACGGCGCGG 120
 1 M ¹ ² A Q P Q R L ¹ F I L D G A D 16
 121 ACGAGCTGCCGGCGCTGGGGGGCCCGAGGCGCGCCTGCACAGACCCCTTCGAGGCGG 180
 17 E L P A L G G P E A A F C T D P F E A A 36
 181 CGAGCGGCGCGCGGTGCTAGCGGGCTGCTAGTAAGGCGTCTGCTGCCACGGCCCTCC 240
 37 S G A R V ¹ G G ² S K A L ¹ P T A L L 56
 241 TGTGCTGACACGCGCGCCCGCCCGGGAGGCTGCAGGGCCGCTGTGTTCCCGCG 300
 57 ¹ V T T R A A A P G R ¹ Q G R L C S P Q 76
 301 AGTGCGCCAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGTATTTCTCAAGTTCT 360
 77 C A E V R G F S D K D K K Y F Y K F F 96
 361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCTGTAAGGAGAACGAGACGCTGT 420
 97 R D E R R A E R A Y R F V K E N E T ¹ F 116
 421 TCGCGTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGTGCGCCAGCAGC 480
 117 A L C F V P F V C W I V C T V ¹ R Q Q L 136
 481 TGGAGCTCGGTGCGGACCTGTGCGCGACGTCCAAGACCAACCGTCAGTGTACCTGCTTT 540
 137 E L G R D L S R T S K T T T S V Y ¹ L F 156
 541 TCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGGCCCGGTTGCAGGCGGACC 600
 157 I T S V L S S A P V A D G P R L Q G D ¹ 176
 601 TCGCAATCTGTGCCGCTGGCCCGGAGGGCGTCTCGGACGACGGGCGCAGTTTGCCG 660
 177 R N ¹ C R ¹ A R E G V L G R R A Q F A E 196
 661 AGAAGGAACCTGGAGCACTGGAGCTTCGTGGCTCCAAGTGCAGACGCTGTTTCTCAGCA 720
 197 K E ¹ E Q L E L R G S K V Q T L F L S K 216
 721 AAAAGGAGCTGCCGGCGTGTGAGACAGAGGTACCTACCAAGTTCATCGACACAGCT 780
 217 K E L P G V L E T E V T Y Q F I D Q S F 236
 781 TCCAGGAGTTCCTCGGGCACTGTCTACCTGCTGGAGACGGCGGGGTGCCAGGACCG 840
 237 Q E F L A A L S Y L ¹ E D G G V P R T A 256
 841 CGGCTGGCGGCTGGGACACTCTGCTGGGGAGCGCCAGCCGACAGCCACTTGGTGC 900
 257 A G G V G T L L ¹ R G D A Q P H S H L V L 276

901	TCACCACCGCGCTTCTCTTCGGA	TGCTGAGCGCGGAGCGGATGCGGCACATCGAGCGCC	960
277	T T R F L F G <u>U</u> L S A E R M R D I E R H		296
961	ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTCGCGTGGGTGCAGGGAC		1020
297	F G <u>C</u> M V S E R V K Q E A L R W V Q G Q		316
1021	AGGGACAGGGCTGCCCGGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG		1080
317	G Q G C F G V A F E V T E G A K G L E D		336
1081	ACACCGAAGAGCCAGAGGAGGAGGAGGAGGAGGAGGCCCAACTACCACTGGAGTTGC		1140
337	T E E P E E E E E G E E P N Y P L E L <u>U</u>		356
1141	TGTACTGCGTGTACGAGAGCGCAGGAGGACCGCTTTGTGCGCAAGCCCTGTGCGCGTTCC		1200
357	Y <u>C</u> <u>U</u> Y E T Q E D A F V R Q A L C R F P		376
1201	CGGAGCTGGGCGTGCAGCGAGTGCCTTCTGCCGATGGACGTGGCTGTTCTGAGCTACT		1260
377	E L A L Q R V R F C R M D V A V L S Y <u>C</u>		396
1261	CGGTGAGGTGCTGCCCTGCTGGACAGGCACCTGGCGCTGATCAGCTGCAGATTGGTTGCTG		1320
397	V R C C P A G Q A L R <u>U</u> I S C R L V A A		416
1321	CGCAGGAGAAGAAGAAGAGCGCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGGCA		1380
417	Q E K K K K S <u>U</u> G K R L Q A S L G G G S		436
1381	GTTCTCAAGGCACCAAAACAACCTGCAGCGCTCCCTTCTTCATCCACTCTTTGAGGCAA		1440
437	S Q G T T T K Q <u>U</u> P A S L L H P L F Q A M		456
1441	TGACTGACCCACTGTGCCACTCTGAGCAGCCTCAGCGTGTCCCACTGCAAACTCCCTGAGC		1500
457	T D P L <u>C</u> H <u>U</u> S S L T L S H C K L P D A		476
1501	CGGTCTGCCGAGACCTTTCTGAGGCGCTGAGGCGAGCCCCGCACTGACGGAGCTGGGCC		1560
477	V C R D L S E A <u>U</u> R A A P A L T E <u>U</u> G <u>U</u>		496
1561	TCCTCCACAACAGGCTCAGTGAGGCGGAGTGCATGTGCTGAGTGAGGGCTAGCGCTGGC		1620
497	L H N R L S E A G L R M <u>U</u> S E G L A W P		516
1621	CGCAGTGCAGGGTCGAGACGGTCAGGTCAGAGTGCCTGACCCCGCAGCGAGGGCTCCAGT		1680
517	Q <u>C</u> R V Q T V R V Q L P D P Q R G L Q Y		536
1681	ACCTGGTGGGTATGCTTCGGCAGAGCCCGCCCTGACCAACCTGGATCTCAGCGGCTGCC		1740
537	<u>U</u> V G M <u>U</u> R G S P A <u>U</u> T T L D <u>U</u> S G C Q		1760
1741	AACCTGCGCGCCCCCATGGTGACCTACCTGTGTGCACTGTCAGCAGCAGGGATGCGGCC		1800
557	T P A P M V T Y L L C A V <u>U</u> Q H Q G <u>C</u> G L		576

Figure 1C

[illegible]

Figure 2A

	1	50
HLRHS11	(1)	-----
caspase_recruitment_protein	(1)	MAAGAWGRLVAVLAKKELKELKANKAHSSSSSGETPPKPKSSK
crpyopyrin	(1)	-MASTRCNLAVLADVDVKKKFMHEDYKQGCIPKRCQCKKACH
Nucleotide_Binding_site	(1)	---MGFNLCALKQSCQKSKKFFVLTITTSKAELOKPKKPKVKAAG
	51	100
HLRHS11	(1)	-----
caspase_recruitment_protein	(51)	KEVQVYFACVQSGKRLQALAHKGLKELKALAGHSPKFTKQ
crpyopyrin	(50)	YLLKMMTFQSGKAWAKNTALKADYKALKEPEKWSQNAHV
Nucleotide_Binding_site	(47)	KQVETLTTRCHSYWQMAKQWSPKQKQSDKAEKVEVRKALKSNK
	101	150
HLRHS11	(1)	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQPTSTAVLMPWIHELPAQCQGSERRVRLQPLTSGRRWRE
crpyopyrin	(100)	SN-----
Nucleotide_Binding_site	(97)	RR-----
	151	200
HLRHS11	(1)	-----
caspase_recruitment_protein	(151)	ISASHLYQALPSSPDHSPSQESPNAPTSTAVLGSMGSPFOSSAPRQOE
crpyopyrin	(102)	-----ETVTCQSDS
Nucleotide_Binding_site	(99)	-----LISLGITR
	201	250
HLRHS11	(1)	-----
caspase_recruitment_protein	(201)	APGTCWVQEPGSGIVYITPRERISSTKPPFAAVVGTTPKSHSLSP
crpyopyrin	(111)	ISEEWKQLEKTSISCKMRKMSPKRYKYSFCCIDMRKLGESLV
Nucleotide_Binding_site	(107)	KRPFLQVDEEIPERNTACQKDKNCBILITKPKFENMKWSKDSKELQW
	251	300
HLRHS11	(1)	-----
caspase_recruitment_protein	(251)	HHHPPPSVQKELCSTWPKWKNDFNQKFTQLLLLRKHPRASODPLVKRSW
crpyopyrin	(161)	SLAKVITLGLKKEHRSQGEHDELLAIGKTKCESLV-----
Nucleotide_Binding_site	(157)	MAKPKMLLPKSPR-----
	301	350
HLRHS11	(1)	-----
caspase_recruitment_protein	(301)	PDYVEENRGHLETRDLFGPGIDTQEPHIVLQGAAGIGKSTLARQVKEA
crpyopyrin	(199)	-----SPKMKELLFDPDDEHSEPVRITVIVCGAAGIGKTLARQVLLD
Nucleotide_Binding_site	(172)	-----VLPGFPSHTVIVLSPAGSKRTLLKMLD
	351	400
HLRHS11	(1)	-----
caspase_recruitment_protein	(351)	MGHGLYQDRFQHVYSCRELQSKVYSLAELGKGGHATPAPTRQITIN
crpyopyrin	(241)	WASGLYQDRFQHVYHREASLVTRQSDGLDMCCQTPNPPHTRIVR
Nucleotide_Binding_site	(202)	WAKNTHSRQKQETSCRELQKSGPCSAELNFMVHMLQDTPHIL
	401	450
HLRHS11	(4)	-----
caspase_recruitment_protein	(401)	QKSEGLIDQDEPPALGKQKAPPTPTKASARVLQKSLSNATL
crpyopyrin	(291)	TKSEGLIDQDEPPALGKQKAPPTPTKASARVLQKSLSNATL
Nucleotide_Binding_site	(251)	QARKLELVADQFDELQAFALKEKQKQDPRKQVPTVLSGLNRVLLP
	451	500
HLRHS11	(53)	-----
caspase_recruitment_protein	(451)	TALEKLTAAAGPGLQGRKCSQCAEYGFSGSKKRSYKSGRDEKA
crpyopyrin	(341)	KASGLKLTAAAGPGLQGRKCSQCAEYGFSGSKKRSYKSGRDEKA
Nucleotide_Binding_site	(301)	KASGLKLTAAAGPGLQGRKCSQCAEYGFSGSKKRSYKSGRDEKA
	501	550
HLRHS11	(103)	-----
caspase_recruitment_protein	(501)	IRAFELVRSKRPDALCHVWWSLQALQVQCKRRKPEITLTKSTTTM
crpyopyrin	(391)	RAASELIGKRVHVDKTHPLVCKIVCTSLQKQKESKSLACKSTTDM
Nucleotide_Binding_site	(351)	KRAFELVRSKRPDALCHVWWSLQALQVQCKRRKPEITLTKSTTTM
	551	600
HLRHS11	(153)	-----
caspase_recruitment_protein	(551)	CHLIDAVAKQK-----GPKQLRDLCSLAAGIKQKRLDPPDLPRH
crpyopyrin	(441)	WVFTLSLQPRGGSQHGCKHNGCSLAAGIKQKRLDPPDLPRH
Nucleotide_Binding_site	(401)	SRFTLSLQPRGGSQHGCKHNGCSLAAGIKQKRLDPPDLPRH

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[illegible]

THEORY

Figure 2C

		1201	1250
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1094)	ENSLYRQDIPVAGSIRWPNGLCSTV	REAVTVIEIFCVWDQFLGEINPQH
cryopyrin	(1022)	ENSLYRQDIPVAGSIRWPNGLCSTV	REAVTVIEIFCVWDQFLGEINPQH
Nucleotide_Binding_site	(1008)	ENSLYRQDIPVAGSIRWPNGLCSTV	REAVTVIEIFCVWDQFLGEINPQH
		1251	1300
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1144)	SWMVAGPLLDITRAEPGAVEAVHLPHFVALQGGHVDTSLFQVAHFKEEGML	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1301	1350
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1194)	LEKPARVELHHIVLENPSFSLGVLLKMIHNALRFIPVTSVLLYHRLHP	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1351	1400
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1401	1450
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1294)	DKKDETAVWEALVKGQDLMPATTLIPACIAVPSPLDAPQLLHFVDQYRE	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1451	1500
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1344)	QLIARVTSVEVVLDELHGQVLSQEYERVLAENTRPSQMRKLFSLSQSWD	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----
		1501	1536
HLRRSII	(626)	-----	-----
caspase_recruitment_protein	(1394)	RKCKDGLYQALKETEPHLIMELWEGSKKGLLPLSS	-----
cryopyrin	(1035)	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----

Figure 3

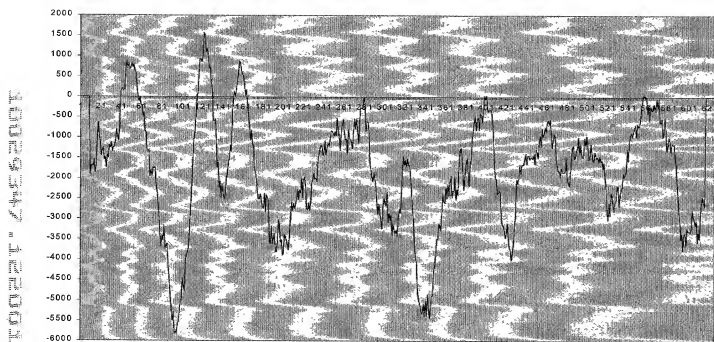


Figure 4

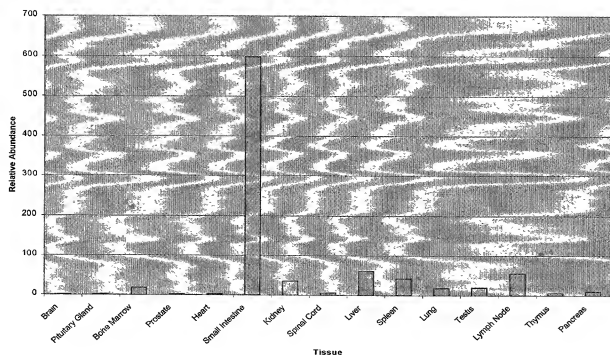


Figure 5.

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%